

MAR. -22' 04 (MON) 18:16

ALSTON & BIRD

TEL:9198622260

P. 027

In re: Mahajan et al..  
Appl. No. 09/954,950  
Filed September 18, 2001

### **APPENDIX TAB 3**

GAP of: 1285AP003238MLH1aa check: 4284 from: 1 to: 715

WPDEF Case 1285 Rice MLH1 protein encoded by genomic cda from GenBank  
AP003238

Rice chromosome 1

Case 1285 Rice MLH1 protein encoded by genomic cda from GenBank  
AP003238 Rice

chromosome 1

ANNOTATED AS MLH1 4/13/02.

Join(33330 .33566,33690 .33862,33943 .34015,34105 .34239, . . .

to: 1285sid2 check: 8164 from: 1 to: 724

WPDEF Case 1285 MLH-1 SEQ ID NO:2 O. sativa

Case 1285 MLH-1 SEQ ID NO:2 O. sativa

Symbol comparison table: blosum62.cmp CompCheck: 1102

BLOSUM62 amino acid substitution matrix.

Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid  
substitution matrices from protein blocks. Proc. Natl.  
Acad.

Sci. USA 89: 10915-10919.

Gap Weight:	8	Average Match:	2.778
Length Weight:	2	Average Mismatch:	-2.248

Quality:	3639	Length:	725
Ratio:	5.090	Gaps:	1
Percent Similarity:	99.860	Percent Identity:	99.860

Match display thresholds for the alignment(s):

| = IDENTITY  
: = 2  
. = 1

1285AP003238MLH1aa x 1285sid2 March 9, 2004 15:35 ..

```
1 MDEPSPRQGGCAGEPPRIRRLSESVVNRIAAGEVIQRPSSAVKELIENSI 50
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MDEPSPRQGGCAGEPPRIRRLSESVVNRIAAGEVIQRPSSAVKELIENSI 50

51 DAGASSVSVAVKDGGLKLIQVSDDGHGIRFEDLAILCERHTTSKLSAYED 100
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 DAGASSVSVAVKDGGLKLIQVSDDGHGIRFEDLAILCERHTTSKLSAYED 100

101 LQTIKSMGFRGEALASMTYVGHVTVTTITBCQLHGYRVSYRDGVMEENPK 150
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 LQTIKSMGFRGEALASMTYVGHVTVTTITBCQLHGYRVSYRDGVMEENPK 150

151 PCAAVKQTOVMVENLFYNMVARKKTLQNSNDDYPKIVDFISRFVHHINV 200
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 PCAAVKQTOVMVENLFYNMVARKKTLQNSNDDYPKIVDFISRFVHHINV 200

201 TFSCRKHGANRADVHSASTSSRLDAIRSVYGASVVRDLIEIKVSYEDAAD 250
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 TFSCRKHGANRADVHSASTSSRLDAIRSVYGASVVRDLIEIKVSYEDAAD 250
```

251 SIFKMDGYISNANYVAKKITMILFINDRLVDCTALKRAIEFVYSATLPQA 300  
|||||  
251 SIFKMDGYISNANYVAKKITMILFINDRLVDCTALKRAIEFVYSATLPQA 300  
301 SKPFTYMSIHLPSHVVDVNIHPTKKEVSLNQERI IETIRNAIEEKLMS 350  
|||||  
301 SKPFTYMSIHLPSHVVDVNIHPTKKEVSLNQERI IETIRNAIEEKLMS 350  
351 NTTRIFQTQALNLSGIAQANPQKDKVSEASMOSGTSQKIPVSQMVRTDP 400  
|||||  
351 NTTRIFQTQALNLSGIAQANPQKDKVSEASMOSGTSQKIPVSQMVRTDP 400  
401 RNPSGRLHTYWHGQSSNLEKKFDLVSVRNVRNRRNQKDAQDLSSRHELL 450  
|||||  
401 RNPSGRLHTYWHGQSSNLEKKFDLVSVRNVRNRRNQKDAQDLSSRHELL 450  
451 VEIDSSFPGLLDIVKNCTYVGLADEAFALIQHNTRLVNVVNISKELM 500  
|||||  
451 VEIDSSFPGLLDIVKNCTYVGLADEAFALIQHNTRLVNVVNISKELM 500  
501 YQQALCRFGNFNAIQLSEPAPLQELLVMALKDDELMSDEKDEKLEIAEV 550  
|||||  
501 YQQALCRFGNFNAIQLSEPAPLQELLVMALKDDELMSDEKDEKLEIAEV 550  
551 NTEILKENAEMINBYFSIHIDQDGKLTRLPVVLDQYTPDMDRLPEFVLAL 600  
|||||  
551 NTEILKENAEMINBYFSIHIDQDGKLTRLPVVLDQYTPDMDRLPEFVLAL 600  
601 GNDVTWDDKEKCFRTVASAVGNFYALHPPILPNPSONGIHLYKKNRDSMA 650  
|||||  
601 GNDVTWDDKEKCFRTVASAVGNFYALHPPILPNPSONGIHLYKKNRDSMA 650  
651 DEHAENDLISDENPVDQELLAEFAAWAQREWTHQVLFPSMRLFLKPPK 700  
|||||  
651 DEHAENDLISDENPVDQELLAEFAAWAQREWTHQVLFPSMRLFLKPPK 700  
701 SMATDGTFFVQVPSDL..... 715  
|||||  
701 SMATDGTFFVQVAS.LEKLYKIFERC 724

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## **APPENDIX TAB 4**